

FIG. 1
(SEQ. ID NO: 1 & 2)

10	20	30	40	50	60	70	80	90
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
ATGCTTTGG AACAGACCA GTCACAGAT TATTATTG AGCAATGCA ATGATGTC ACTATGCT ACAGTCATA TGAATCATC								90
M A L E Q N Q S T D Y Y Y E E N E M N G T Y D Y S Q Y E L I								
180								
TGATCAAG AAGATGAC AGATTTTCC TACTGTTAT TCTCAGATA GTTTTGCA TTGACATTC AGCAATTC								
C I K E D V R E F A K V F L P V F L T I V F V I G L A G N S								
270								
ATGCTAGGG CATTTATTC CTATTCAAG AACAGAGAA CCAAAAGCA TGTGACATC CTAATTTGG CTTAGACCA TTACTCTTT								
M V V A I Y A Y Y K K Q R T K T D V Y I L N L A V A D L L L								
360								
CTATTCATC TACTTTTGG GCTGTTAT GCGATTCAG GCTGCTTTT AGCAATTA ATGTCATA TAACTTCACC CTGTCACA								
L F T L P F W A V N A V H G W V L G K I M C K I T S A L Y T								
450								
CTAACTTTC TCTCTCAT CCAATTTTC GCTTGATCA CCAATGACAG ATGTCGCA GPACTAAG TCTTCAGCA ATCAGAGTG								
L N F V S G M Q F L A C I S I D R Y V A V T K V P S Q S G V								
540								
GGAAACCT CCTGATCAT CAGTTCTGT GCTGATGG CTGCACTT GCTGAGTA CCAATGTC TTTTATTC AGTAAATGC								
G K P C W I I C F C V W M A A I L L S I P Q L V F Y T V N D								
630								
ATGCTAGCT CATCTCAT TTTCTTGG TACTGAGA CATATGAA AGCTTAT CAAATCTAG AGATCTCAT TCAATTTGTA								
N A R C I P I F P R Y L G T S M K A L I Q M L E I C I G F V								
720								
GTACCTTC TTTATGG GCTGCTAC TTTATCAG CAGCACT CATGAGTG CCAATCTA AATATCTAG ACCCTAATA								
V P F L I M G V C Y F I T A R T L M K M P N I K I S R P L K								
810								
GTCTCTCA CAGCTTAT AGTTTAT GTACTAAC TGGCTTGA CATTTCAAG TTTCTGAG CATTAGCT CATCTCTC								
V L L T V V I V F I V T Q L P Y N I V K F C R A I D I I Y S								
900								
CTGATACA CTTCAACT GAGCAACC ATGCTATG CATTCAAT GACATACC ATCTACT TTTACAGTG CTTCAACCA								
L I T S C N M S K R M D I A I Q V T E S I A L F H S C L N P								
990								
ATCTTTAG TTTTATGG AGATCTTC AAAATCTAG TTTGAAAT GCTCAAGAA TATCTGCT GAGAGACA GAGCAATGT								
I L Y V F M G A S F K N Y V M K V A K K Y G S W R R Q R Q S								
1080								
GTGAGAGT TTTCTTGA TTTGAGGT CTTACAGC CAACTGAC TTTTCAAT TAAAGTAA ACTCTCTC CTTTCTTG								
V E E F P F D S E G P T E P T S T F S I . R . N C S A F C L								
1147								
GATCATAG ATGCTCTT TCTCTAAA TAAATCTT GCTTATCT GAAAAAAA AAAAAM								
D T Y E . C F P L K . N I C L I L K K K K K								

A

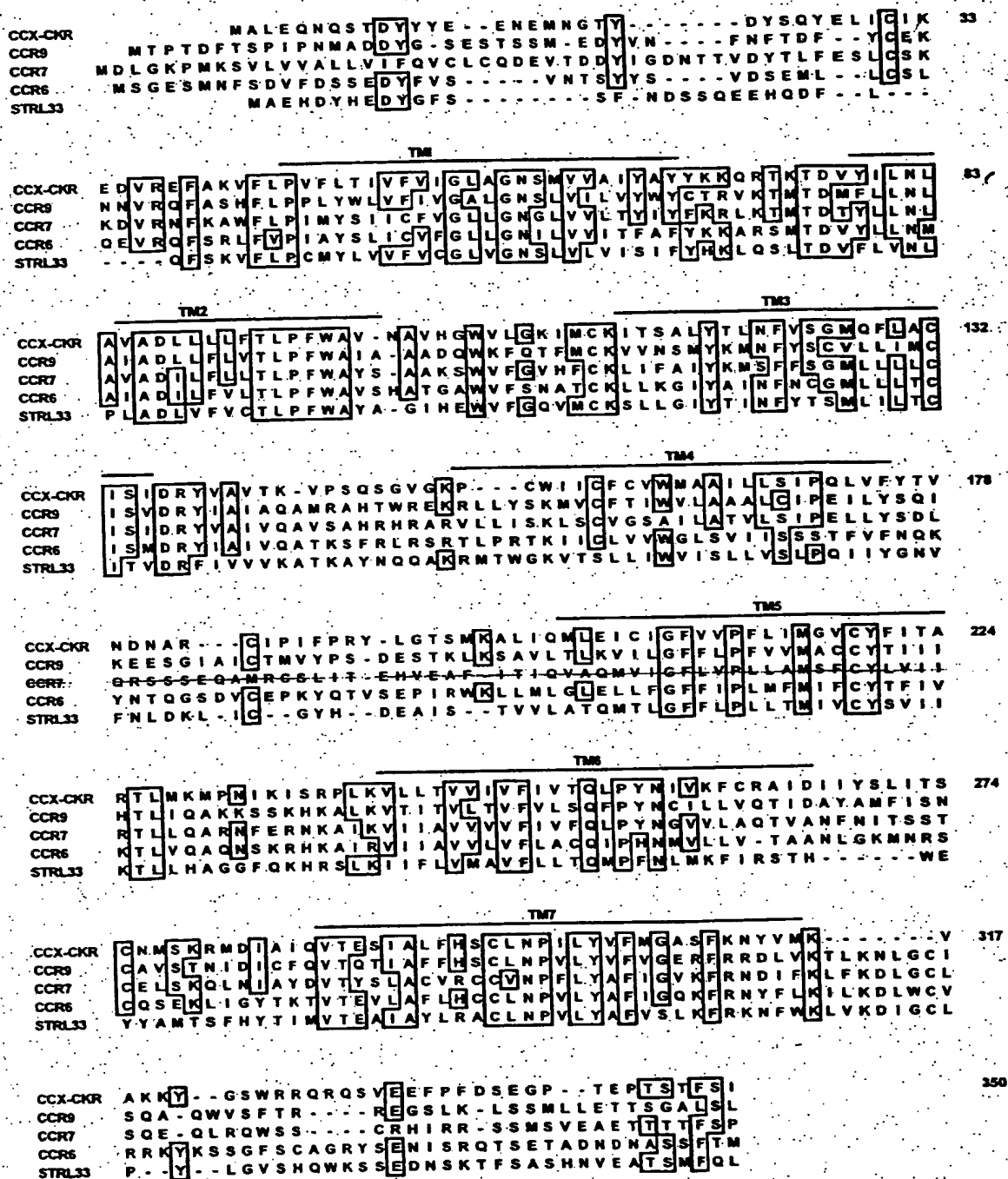


FIG. 2(a)

001211" 56H12260

B

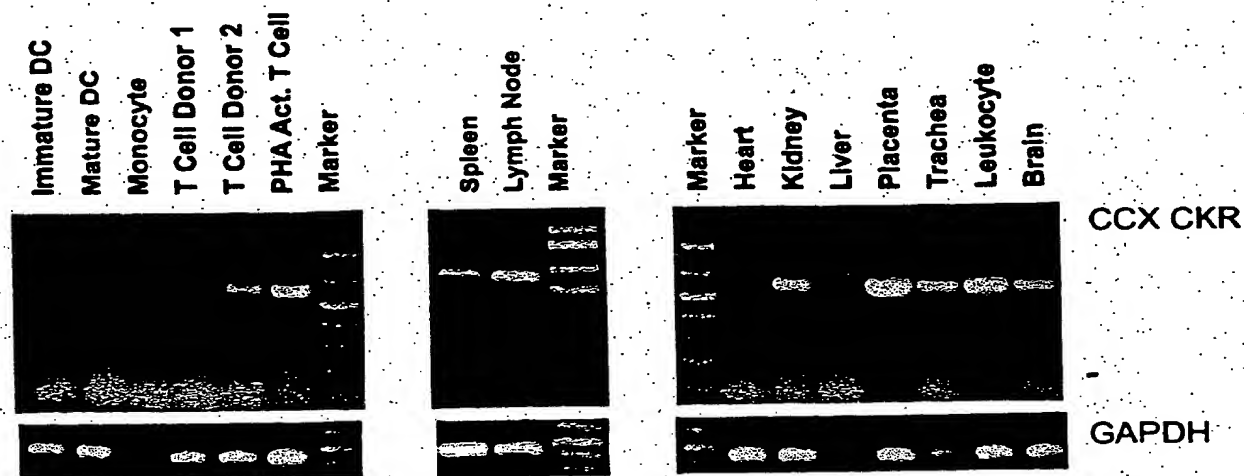


FIG. 2(b)

C

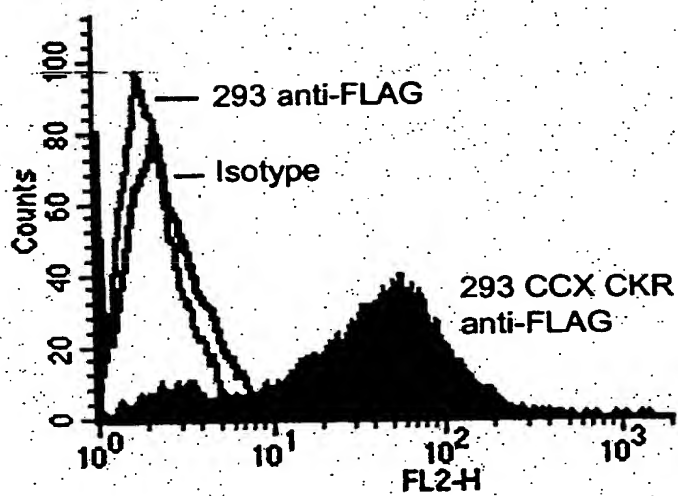
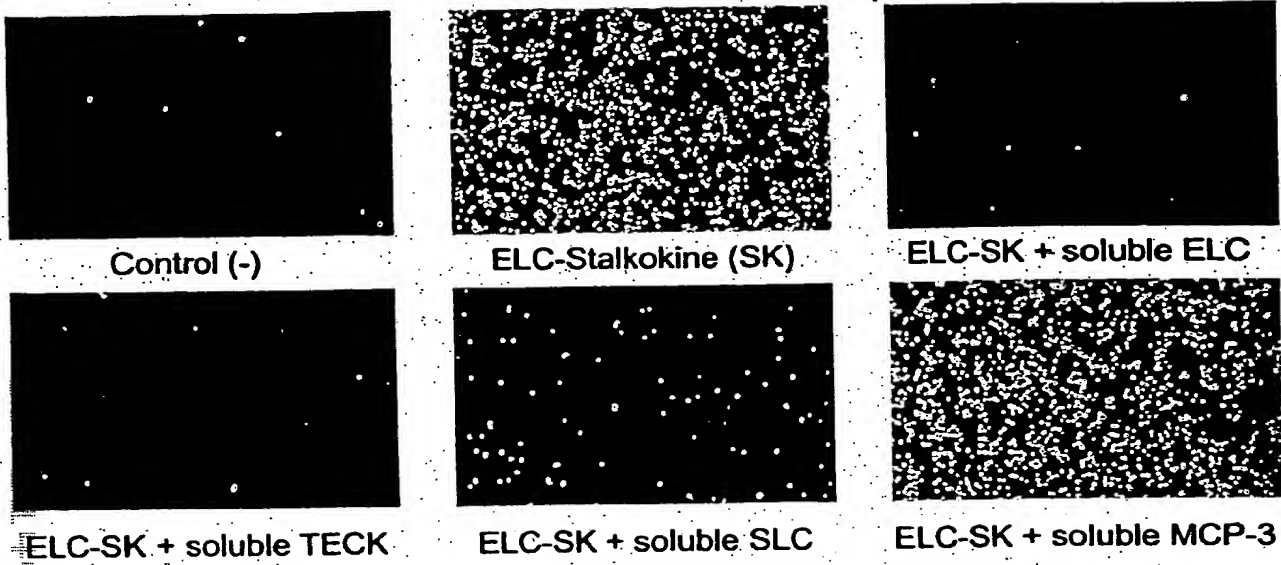


FIG. 2(c)

FIG. 3(a)

A



B

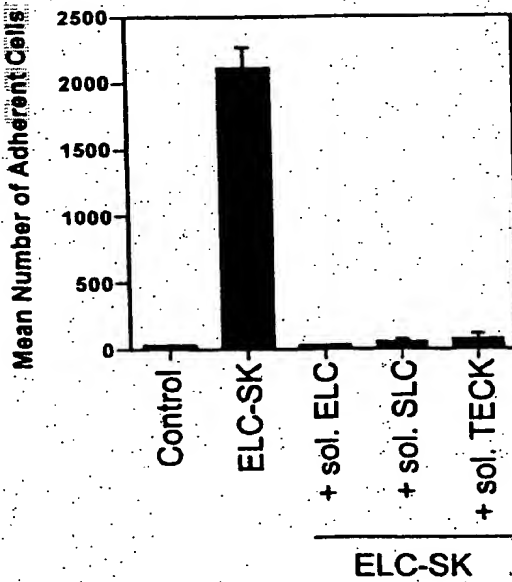


FIG. 3(b)

C

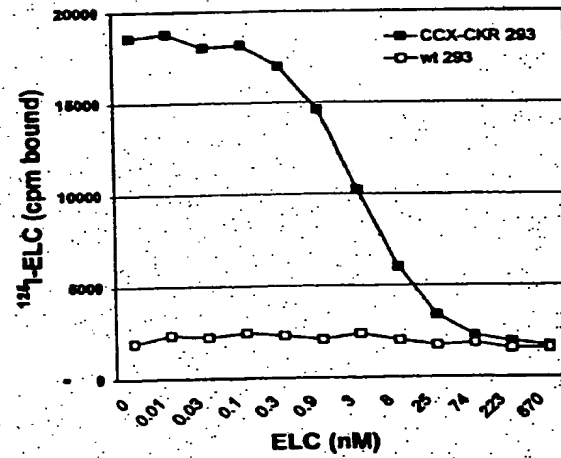


FIG. 3(c)

A

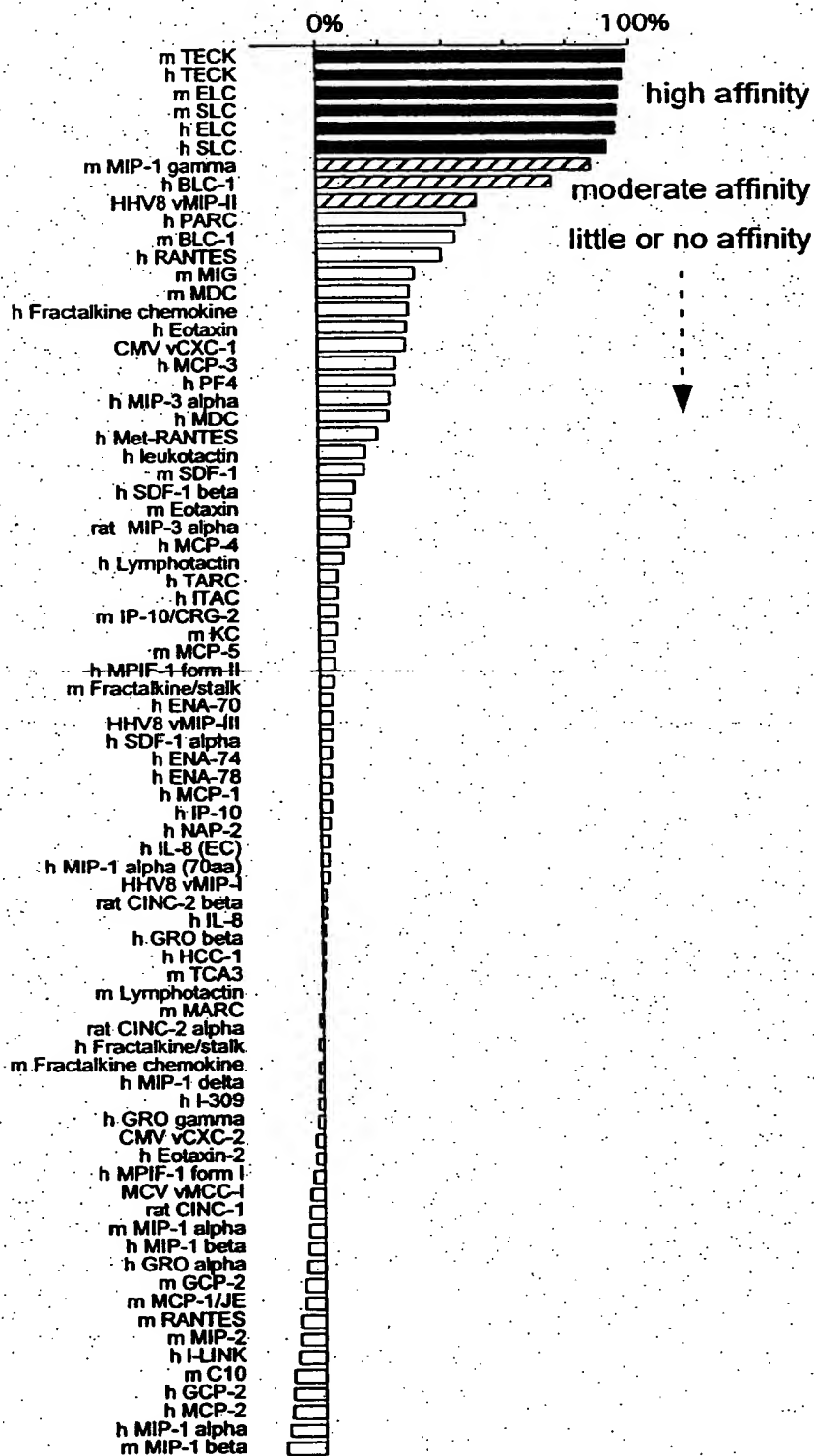
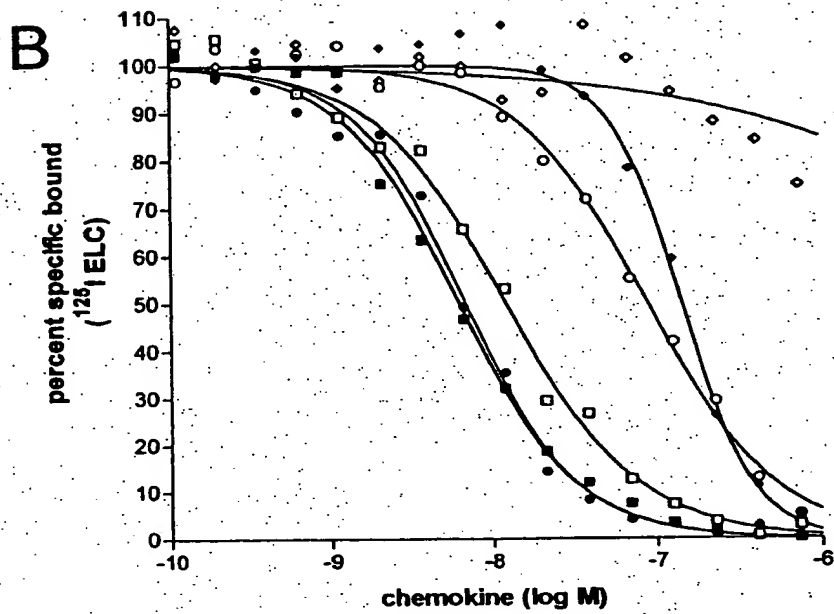
percent inhibition
of ^{125}I -ELC binding

FIG. 4(a)



human chemokines		murine chemokines	
	IC-50		IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
● h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1 γ	70 nM
○ HHV8 wMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4(b)



5' upstream CCXCKR	ATGCAGCATC	TGGTTTATAA	AAGGCAACTA	GTGAAATTTA	GTGCAAATGC	50
5' upstream CCXCKR	TGAGAGAATT	TATTTAACTT	ATTTAAATTA	AATTTATAAA	TAACATCAAA	100
5' upstream CCXCKR	ATAAAAAATA	AATTTAATTT	AAATAAACCA	AGTAATTTGC	TATTTTCGTT	150
5' upstream CCXCKR	TTTATTCAAT	TTGTTGTAGA	TATACITTTA	CGATTCACAA	AATTATGTAT	200
5' upstream CCXCKR	GTAAGATTAA	TAACACTATT	TATTCITTTT	AGTTAAATTC	TAATTAAATT	250
5' upstream CCXCKR	TTTATATTTT	AAAAATCATT	TTTACATAAA	AGTCTTCACT	TTTATTTAGG	300
5' upstream CCXCKR	ATTTAATGAT	TAAGAAAATT	CTCCAGGGCA	TTATGTTTAT	TGTCTGTGTC	350
5' upstream CCXCKR	AAATCCAAGC	TCTTTCACAC	AGAATGTGAC	AAGCAAAGTT	TGAGTAACTA	400
5' upstream CCXCKR	ATCTTGGGGT	CATATTCCAA	TGTGGCTGCC	ATTAAAGCAT	TTCAAAGAGT	450
5' upstream CCXCKR	GCTAGATTCA	GGCTCACATA	TGTTACAGCA	ACAGGCTATA	CTCTAGGGAA	500
5' upstream CCXCKR	AGAACAAAAC	AGCTTGATAG	AAACTGTGTG	CTTTAAGCA	TATTTAGACA	550
5' upstream CCXCKR	AATATCTATC	CIGTATTCIC	TTTGCCATCT	AGATTGGAGC	CATGGCTGTC	600 9
5' upstream CCXCKR	TAAAGAGAGC	CTCTTGGGTT	TTTATTTTTC	TTTATTTTTC	TTTATTTTTC	649 58
5' upstream CCXCKR	CCCTTAAAGC	CTCTTGGGTT	TTTATTTTTC	TTTATTTTTC	TTTATTTTTC	685 108
5' upstream CCXCKR	AGAGAGAGAG	CAGAGGAGAG	TTTATTTTTC	TTTATTTTTC	TTTATTTTTC	734 147
5' upstream CCXCKR	ATTCGTTTTC	TCATTGGACT	TGCAGGCAAT	TCCATGGT	TGGCAATTTA	740 197
5' upstream CCXCKR	TGCCTATTAC	AAGAAACAGA	GAACCAAAC	AGATGTGTAC	ATCCTGAATT	740 247
5' upstream CCXCKR	TGGCTGTAGC	AGATTDACTC	CTTCTATTCA	CTCTGCCTTT	TTGGGCTGTT	740 297
5' upstream CCXCKR	AATGCAGTTC	ATGGGTGGGT	TTTAGGGAAA	ATAATGTGCA	AATAAAGTTC	740 347

Internalization by FACS 45 minute Incubation

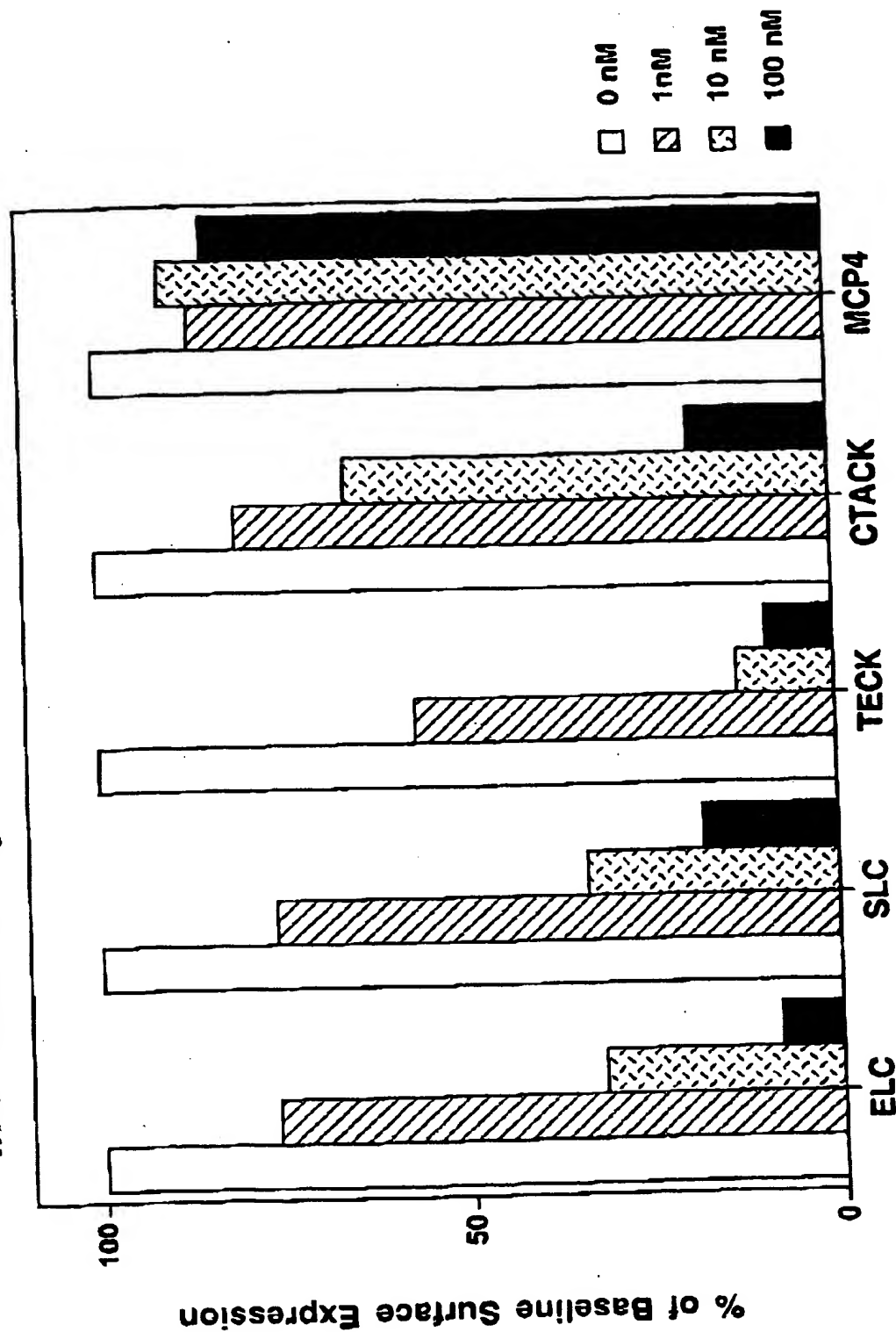


Fig. 6A

Internalization by FACS 15 minute Incubation

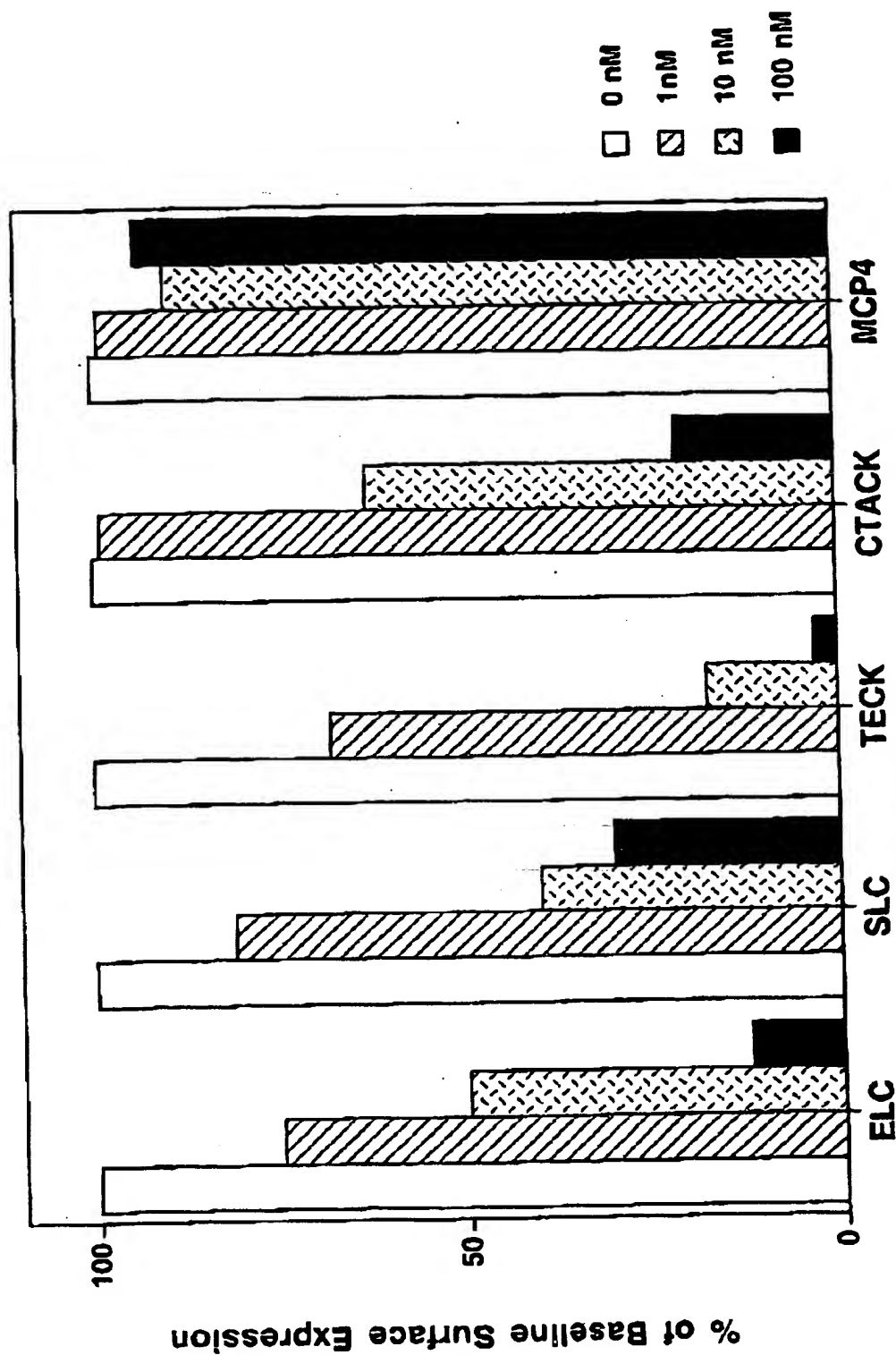


Fig. 6B